

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1656SXC

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 "Ask CAS" for self-help around the clock
NEWS 3 DEC 05 CASREACT(R) - Over 10 million reactions available
NEWS 4 DEC 14 2006 MeSH terms loaded in MEDLINE/LMEDLINE
NEWS 5 DEC 14 2006 MeSH terms loaded for MEDLINE file segment of TOXCENTER
NEWS 6 DEC 14 CA/CAplus to be enhanced with updated IPC codes
NEWS 7 DEC 21 IPC search and display fields enhanced in CA/CAplus with the
IPC reform
NEWS 8 DEC 23 New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
USPAT2
NEWS 9 JAN 13 IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
NEWS 10 JAN 13 New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to
INPADOC
NEWS 11 JAN 17 Pre-1988 INPI data added to MARPAT
NEWS 12 JAN 17 IPC 8 in the WPI family of databases including WPIFV
NEWS 13 JAN 30 Saved answer limit increased
NEWS 14 JAN 31 Monthly current-awareness alert (SDI) frequency
added to TULSA

NEWS EXPRESS JANUARY 03 CURRENT VERSION FOR WINDOWS IS V8.01,
CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
V8.0 USERS CAN OBTAIN THE UPGRADE TO V8.01 AT
<http://download.cas.org/express/v8.0-Discover/>

NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS INTER	General Internet Information
NEWS LOGIN	Welcome Banner and News Items
NEWS PHONE	Direct Dial and Telecommunication Network Access to STN
NEWS WWW	CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

All use of STN is subject to the provisions of the STN Customer agreement. Please note that this agreement limits use to scientific research. Use for software development or design or implementation of commercial gateways or other similar uses is prohibited and may result in loss of user privileges and other penalties.

FILE 'HOME' ENTERED AT 17:18:39 ON 09 FEB 2006

=> FIL CAPLUS

COST IN U.S. DOLLARS

SINCE FILE ENTRY 0.21	TOTAL SESSION 0.21
-----------------------------	--------------------------

FILE 'CAPLUS' ENTERED AT 17:18:49 ON 09 FEB 2006

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA Lexicon is the copyrighted intellectual property of the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS, is strictly prohibited.

FILE COVERS 1907 - 9 Feb 2006 VOL 144 ISS 7
FILE LAST UPDATED: 8 Feb 2006 (20060208/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply. They are available for your review at:

<http://www.cas.org/infopolicy.html>

=> s tgttagccggccacgctgg/sqsn
REGISTRY INITIATED
Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L2 0 L1

=> s taccacgcgacacacttc/sqsn
REGISTRY INITIATED
Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L4 1 L3

=> d 14

L4 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:10074 CAPLUS
DN 136:65204
TI Transgenic corn plant PV-ZMGT32 (nk603) transformed with DNA construct containing 5-enolpyruvoylshikimate 3-phosphate synthase for conferring glyphosate tolerance
IN Behr, Carl F.; Hironaka, Catherine; Heck, Gregory R.; You, Jinsong
PA Monsanto Technology Llc, USA
SO Eur. Pat. Appl., 25 pp.
CODEN: EPXXDW

DT Patent

LA English

FAN. CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1167531	A1	20020102	EP 2001-202314	20010615
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	BR 2001000752	A	20020213	BR 2001-752	20010222
	ZA 2001004092	A	20011119	ZA 2001-4092	20010518
	US 2002013960	A1	20020131	US 2001-872051	20010601

US 6825400	B2	20041130		
EP 1582592	A1	20051005	EP 2005-105879	20010615
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
CA 2349841	AA	20011222	CA 2001-2349841	20010620
CN 1332246	A	20020123	CN 2001-122036	20010622
BG 105637	A	20020430	BG 2001-105637	20010622
US 2004139493	A1	20040715	US 2004-790430	20040301
PRAI US 2000-213567P	P	20000622		
US 2000-240014P	P	20001013		
US 2000-241215P	P	20001013		
US 2001-872051	A3	20010601		
EP 2001-202314	A3	20010615		

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s accaagctttataatag/sqsn

REGISTRY INITIATED

Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L6 1 L5

=> d 16

L6	ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN			
AN	2002:10074 CAPLUS			
DN	136:65204			
TI	Transgenic corn plant PV-ZMGT32 (nk603) transformed with DNA construct containing 5-enolpyruvoylshikimate 3-phosphate synthase for conferring glyphosate tolerance			
IN	Behr, Carl F.; Hironaka, Catherine; Heck, Gregory R.; You, Jinsong			
PA	Monsanto Technology Llc, USA			
SO	Eur. Pat. Appl., 25 pp.			
DT	CODEN: EPXXDW			
LA	Patent			
LA	English			
FAN.CNT 1				
	PATENT NO.	KIND	DATE	APPLICATION NO.
PI	EP 1167531	A1	20020102	EP 2001-202314
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
	BR 2001000752	A	20020213	BR 2001-752
	ZA 2001004092	A	20011119	ZA 2001-4092
	US 2002013960	A1	20020131	US 2001-872051
	US 6825400	B2	20041130	
	EP 1582592	A1	20051005	EP 2005-105879
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
	CA 2349841	AA	20011222	CA 2001-2349841
	CN 1332246	A	20020123	CN 2001-122036
	BG 105637	A	20020430	BG 2001-105637
	US 2004139493	A1	20040715	US 2004-790430
PRAI	US 2000-213567P	P	20000622	
	US 2000-240014P	P	20001013	
	US 2000-241215P	P	20001013	
	US 2001-872051	A3	20010601	
	EP 2001-202314	A3	20010615	

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d his

(FILE 'HOME' ENTERED AT 17:18:39 ON 09 FEB 2006)

FILE 'CAPLUS' ENTERED AT 17:18:49 ON 09 FEB 2006
S TGTAGCGGCCACGCTGG/SQSN

FILE 'REGISTRY' ENTERED AT 17:19:17 ON 09 FEB 2006
L1 0 S TGTAGCGGCCACGCTGG/SQSN

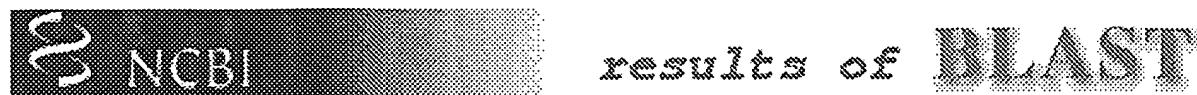
FILE 'CAPLUS' ENTERED AT 17:19:37 ON 09 FEB 2006
L2 0 S L1
S TACCAACGCGACACACTTC/SQSN

FILE 'REGISTRY' ENTERED AT 17:20:40 ON 09 FEB 2006
L3 6 S TACCAACGCGACACACTTC/SQSN

FILE 'CAPLUS' ENTERED AT 17:21:00 ON 09 FEB 2006
L4 1 S L3
S ACCAAGCTTTATAATAG/SQSN

FILE 'REGISTRY' ENTERED AT 17:22:13 ON 09 FEB 2006
L5 8 S ACCAAGCTTTATAATAG/SQSN

FILE 'CAPLUS' ENTERED AT 17:22:35 ON 09 FEB 2006
L6 1 S L5



BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

RID: 1139520495-2564-183997461739.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

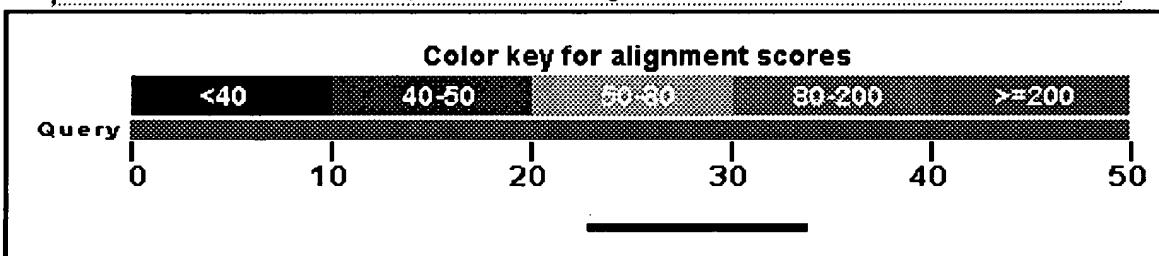
[Taxonomy reports](#)

Query=

Length=50

Distribution of 2 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Sequences producing significant alignments:

gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome 22.3 1.1

Alignments

[Get selected sequences](#)

[Select all](#)

[Deselect all](#)

> gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome
Length=140384

Score = 22.3 bits (11), Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

```
Query  24      AGGGTGAAGTA  34
       |||||||||||||
Sbjct  96767    AGGGTGAAGTA  96777
```

Score = 22.3 bits (11), Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

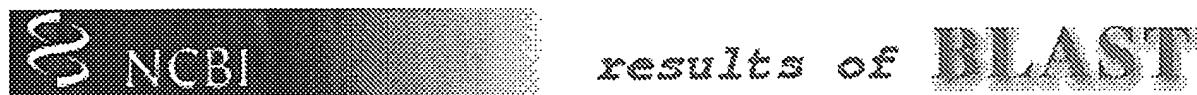
```
Query  24      AGGGTGAAGTA  34
       |||||||||||||
Sbjct  125970   AGGGTGAAGTA  125960
```

[Get selected sequences](#)

[Select all](#)

[Deselect all](#)

Database: NCBI Genomic Reference Sequences
Posted date: Feb 7, 2006 12:38 PM
Number of letters in database: 142,297
Number of sequences in database: 2
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 50
Length of database: 142297
Length adjustment: 11
Effective length of query: 39
Effective length of database: 142297
Effective search space: 5549583
Effective search space used: 5548725
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
S2: 10 (20.3 bits)



BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520495-2564-183997461739.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

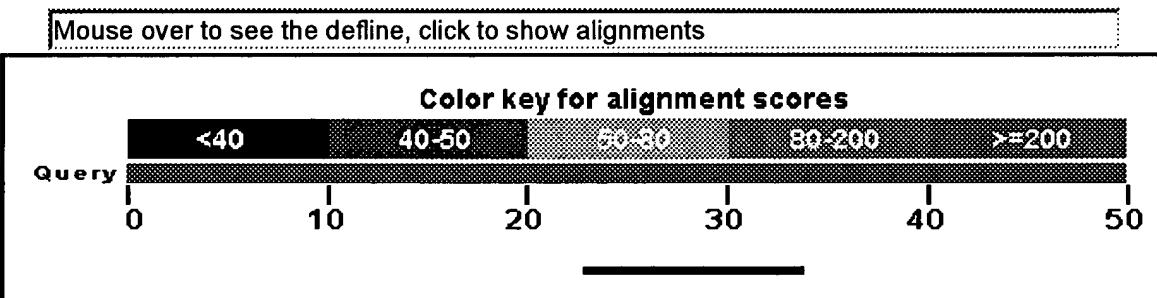
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Query=

Length=50

Distribution of 2 Blast Hits on the Query Sequence



Sequences producing significant alignments:

gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome 22.3 1.1

Alignments

[Get selected sequences](#)

[Select all](#)

[Deselect all](#)

> gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome
Length=140384

Score = 22.3 bits (11), Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

```
Query  24      AGGGTGAAGTA  34
       ||||||||| |
Sbjct  96767   AGGGTGAAGTA  96777
```

Score = 22.3 bits (11), Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

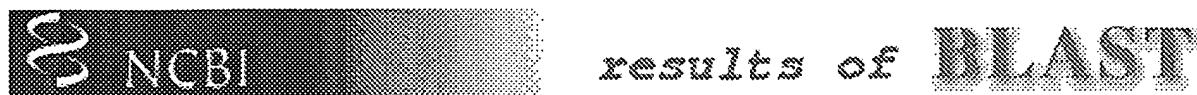
```
Query  24      AGGGTGAAGTA  34
       ||||||||| |
Sbjct  125970   AGGGTGAAGTA  125960
```

[Get selected sequences](#)

[Select all](#)

[Deselect all](#)

Database: NCBI Genomic Reference Sequences
Posted date: Feb 7, 2006 12:38 PM
Number of letters in database: 142,297
Number of sequences in database: 2
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 50
Length of database: 142297
Length adjustment: 11
Effective length of query: 39
Effective length of database: 142297
Effective search space: 5549583
Effective search space used: 5548725
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
S2: 10 (20.3 bits)



BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520711-10093-27750649669.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

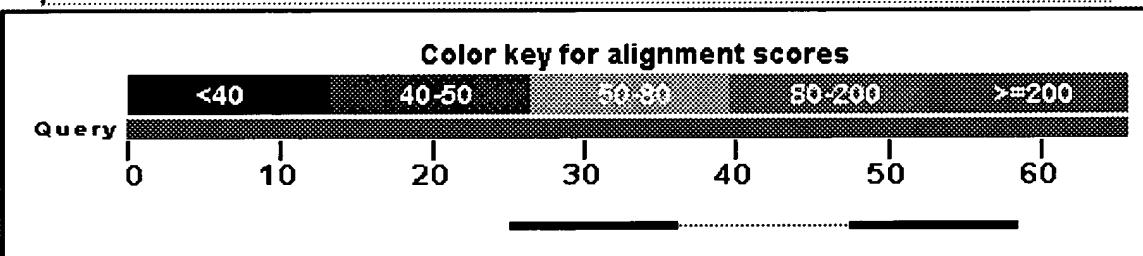
[Taxonomy reports](#)

Query=

Length=65

Distribution of 3 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Score (Bits)	E Value
Sequences producing significant alignments:	
gi 11994090 ref NC_001666.2 Zea mays chloroplast, complete genome	22.3 1.5

Alignments

[Get selected sequences](#) [Select all](#) [Deselect all](#)

> gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome
Length=140384

Score = 22.3 bits (11), Expect = 1.5
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 48 GATCTTTCTC 58
|||||||||||
Sbjct 44568 GATCTTTCTC 44578

Score = 22.3 bits (11), Expect = 1.5
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 26 TCCTCCTCTCT 36
|||||||||||
Sbjct 83760 TCCTCCTCTCT 83770

Score = 22.3 bits (11), Expect = 1.5
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

Query 26 TCCTCCTCTCT 36
|||||||||||
Sbjct 138977 TCCTCCTCTCT 138967

Database: NCBI Genomic Reference Sequences
Posted date: Feb 7, 2006 12:38 PM
Number of letters in database: 142,297
Number of sequences in database: 2
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 65
Length of database: 142297
Length adjustment: 11
Effective length of query: 54
Effective length of database: 142297
Effective search space: 7684038
Effective search space used: 7682850
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520074-12515-142933253334.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

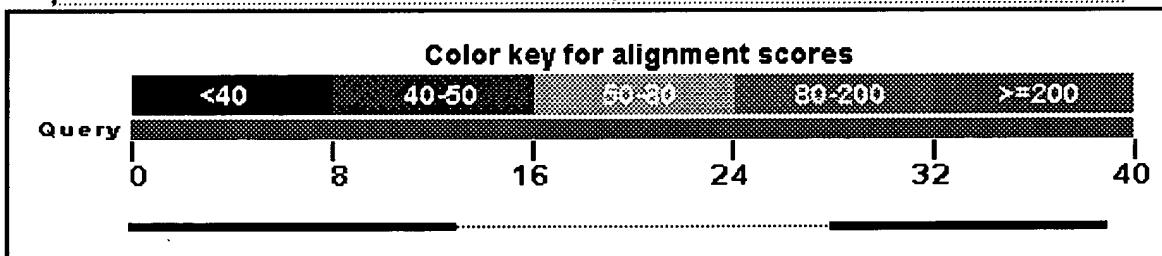
[Taxonomy reports](#)

Query=

Length=40

Distribution of 3 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Sequences producing significant alignments:

Score (Bits)	E Value
--------------	---------

gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome 22.3 0.80

Alignments

[Get selected sequences](#)

[Select all](#)

[Deselect all](#)

> gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome
Length=140384

Score = 22.3 bits (11), Expect = 0.80
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 3 TCGATCCAAAA 13
|||||||||||
Sbjct 66973 TCGATCCAAAA 66983

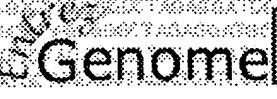
Score = 22.3 bits (11), Expect = 0.80
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 1 AATCGATCCAA 11
|||||||||||
Sbjct 73754 AATCGATCCAA 73764

Score = 22.3 bits (11), Expect = 0.80
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 29 TGGAAGAAAGA 39
|||||||||||
Sbjct 112529 TGGAAGAAAGA 112539

Database: NCBI Genomic Reference Sequences
Posted date: Feb 7, 2006 12:38 PM
Number of letters in database: 142,297
Number of sequences in database: 2
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 40
Length of database: 142297
Length adjustment: 11
Effective length of query: 29
Effective length of database: 142297
Effective search space: 4126613
Effective search space used: 4125975
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)

NCBI   My NCBI
[Sign In] [Regis]

All Databases PubMed Nucleotide Protein Genome Structure PMC Taxonomy Book

Search for

Limits Preview/Index History Clipboard Details

Display Show Send to

All: 1

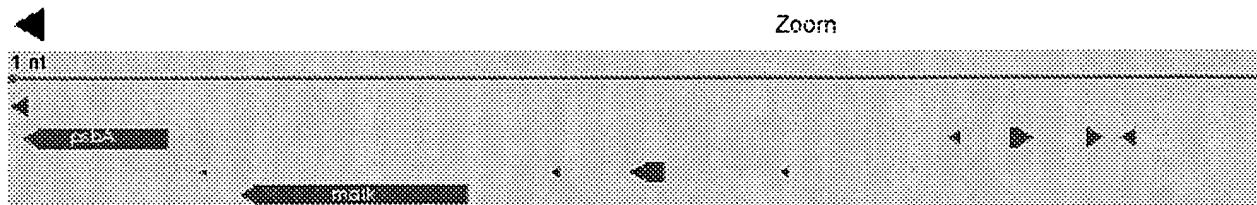
Genome > Eukaryota > Zea mays chloroplast, complete genome

Lineage: Eukaryota ; Viridiplantae ; Streptophytina ; Embryophyta ; Tracheophyta ; Euph
Magnoliophyta ; Liliopsida ; commelinids ; Poales ; Poaceae ; PACCAD clade ; Panicoideae ; Andropog

Genome Info:	Feature table:	BLAST homologs:	Links:	Review:
Refseq: NC_001666	Proteins: 111	COG	Genome Project	Public
GenBank: X86563	Structural RNAs: 47	3D Structure	Refseq FTP	Refseq
Length: 140,384 nt	Genes: 155	TaxMap	GenBank FTP	Seq.S
GC Content: 38%	Others: 153	TaxPlot	BLAST	Seque
Topology: circular	Total: 466	GenePlot	TraceAssembly	Comp
Molecule: DNA	Contigs: 1	gMap	CDD	Organ
Gen.Code: 1			Other genomes for species	

Gene Classification based on COG functional categories

Search gene, GenelID or locus_tag:



Comment and suggestions to: [\[info@ncbi.nlm.nih.gov\]](mailto:[info@ncbi.nlm.nih.gov])

Display Show Send to



Results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520074-12515-142933253334.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

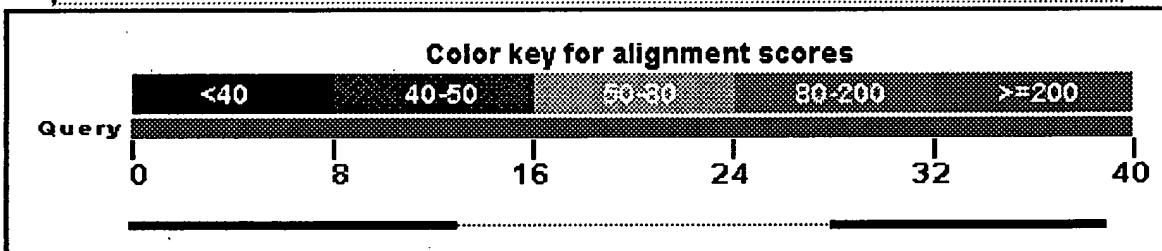
[Taxonomy reports](#)

Query=

Length=40

Distribution of 3 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Sequences producing significant alignments:

Score (Bits)	E Value
--------------	---------

gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome 22.3 0.80

Alignments

[Get selected sequences](#)

[Select all](#)

[Deselect all](#)

> gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome
Length=140384

Score = 22.3 bits (11), Expect = 0.80
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 3 TCGATCCAAAA 13
|||||||||||
Sbjct 66973 TCGATCCAAAA 66983

Score = 22.3 bits (11), Expect = 0.80
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 1 AATCGATCCAA 11
|||||||||||
Sbjct 73754 AATCGATCCAA 73764

Score = 22.3 bits (11), Expect = 0.80
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 29 TGGAAAGAAAGA 39
|||||||||||
Sbjct 112529 TGGAAAGAAAGA 112539

Database: NCBI Genomic Reference Sequences
Posted date: Feb 7, 2006 12:38 PM
Number of letters in database: 142,297
Number of sequences in database: 2
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 40
Length of database: 142297
Length adjustment: 11
Effective length of query: 29
Effective length of database: 142297
Effective search space: 4126613
Effective search space used: 4125975
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)